

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/467, 368A
Source: IFW16
Date Processed by STIC: 02/22/2007

ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/467,368A

DATE: 02/22/2007

TIME: 08:47:53

Input Set : N:\Crf3\RULE60\09467368.RAW
Output Set: N:\CRF4\02222007\I467368A.raw

59 (B) STRAIN: DSM 4109
 61 (ix) FEATURE:
 62 (A) NAME/KEY: CDS
 63 (B) LOCATION: 31..705
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 67 TCGGGCCCGAC GTCTTGCAT CCTTGCAAGTG ATG GTC GGC TTT ACC CCC GTT GCC 54
 68 Met Val Gly Phe Thr Pro Val Ala
 69 1 5
 71 CTT GCG GCC TTA GCC GCG ACT GGG GCC CTG GCC TTC CCG GCA GGG AAT 102
 72 Leu Ala Ala Leu Ala Ala Thr Gly Ala Leu Ala Phe Pro Ala Gly Asn
 73 10 15 20
 75 GCC ACG GAG CTC GAA AAG CGA CAG ACA ACC CCC AAC TCG GAG GGC TGG 150
 76 Ala Thr Glu Leu Glu Lys Arg Gln Thr Thr Pro Asn Ser Glu Gly Trp
 77 25 30 35 40
 79 CAC GAT GGT TAT TAC TAT TCC TGG TGG AGT GAC GGT GGA GCG CAG GCC 198
 80 His Asp Gly Tyr Tyr Ser Trp Trp Ser Asp Gly Gly Ala Gln Ala
 81 45 50 55
 83 ACG TAC ACC AAC CTG GAA GGC GGC ACC TAC GAG ATC AGC TGG GGA GAT 246
 84 Thr Tyr Thr Asn Leu Glu Gly Thr Tyr Glu Ile Ser Trp Gly Asp
 85 60 65 70
 87 GGC GGT AAC CTC GTC GGT GGA AAG GGC TGG AAC CCC GGC CTG AAC GCA 294
 88 Gly Gly Asn Leu Val Gly Gly Lys Trp Asn Pro Gly Leu Asn Ala
 89 75 80 85
 91 AGA GCC ATC CAC TTT GAG GGT GTT TAC CAG CCA AAC GGC AAC AGC TAC 342
 92 Arg Ala Ile His Phe Glu Gly Val Tyr Gln Pro Asn Gly Asn Ser Tyr
 93 90 95 100
 95 CTT GCG GTC TAC GGT TGG ACC CGC AAC CCG CTG GTC GAG TAT TAC ATC 390
 96 Leu Ala Val Tyr Gly Trp Thr Arg Asn Pro Leu Val Glu Tyr Tyr Ile
 97 105 110 115 120
 99 GTC GAG AAC TTT GGC ACC TAT GAT CCT TCC TCC GGT GCT ACC GAT CTA 438
 100 Val Glu Asn Phe Gly Thr Tyr Asp Pro Ser Ser Gly Ala Thr Asp Leu
 101 125 130 135
 103 GGA ACT GTC GAG TGC GAC GGT AGC ATC TAT CGA CTC GGC AAG ACC ACT 486
 104 Gly Thr Val Glu Cys Asp Gly Ser Ile Tyr Arg Leu Gly Lys Thr Thr
 105 140 145 150
 107 CGC GTC AAC GCA CCT AGC ATC GAC GGC ACC CAA ACC TTC GAC CAA TAC 534
 108 Arg Val Asn Ala Pro Ser Ile Asp Gly Thr Gln Thr Phe Asp Gln Tyr
 109 155 160 165
 111 TGG TCG GTC CGC CAG GAC AAG CGC ACC AGC GGT ACC GTC CAG ACG GGC 582
 112 Trp Ser Val Arg Gln Asp Lys Arg Thr Ser Gly Thr Val Gln Thr Gly
 113 170 175 180
 115 TGC CAC TTC GAC GCC TGG GCT CGC GCT GGT TTG AAT GTC AAC GGT GAC 630
 116 Cys His Phe Asp Ala Trp Ala Arg Ala Gly Leu Asn Val Asn Gly Asp
 117 185 190 195 200
 119 CAC TAC TAC CAG ATC GTT GCA ACG GAG GGC TAC TTC AGC AGC GGC TAT 678
 120 His Tyr Tyr Gln Ile Val Ala Thr Glu Gly Tyr Phe Ser Ser Gly Tyr
 121 205 210 215
 123 GCT CGC ATC ACC GTT GCT GAC GTG GGC TAAGACGCTAA CCTGGTGGTG 725
 124 Ala Arg Ile Thr Val Ala Asp Val Gly

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125	220	225	
127	ATCTCGCGAG GCAACAGCCA AGAACATGTCGT CAGATGTGCC GGTTGAAGGT ATTCAATCAG		785
129	CATATCTGTC TGCCCTTGCAG AGTGATACTT TGGAGGACTG TGGAGAACTT TGTGCGAGCC		845
131	TGGCCAGGAT CAGTAGTTGC TTTGCGGTGT TTTGCTCCCT ATTCTCGTGA AAAAATTGTT		905
133	ATTGCTTCGT TGTCTAGTGT ACATAGCCGA GCAATTGAGG CCTCACGCTT GGGAAAAAAA		965
135	AAAAAAAAA AAAAAAAA		983
137	(2) INFORMATION FOR SEQ ID NO: 2:		
139	(i) SEQUENCE CHARACTERISTICS:		
140	(A) LENGTH: 225 amino acids		
141	(B) TYPE: amino acid		
142	(D) TOPOLOGY: linear		
144	(ii) MOLECULE TYPE: protein		
146	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:		
148	Met Val Gly Phe Thr Pro Val Ala Leu Ala Ala Leu Ala Ala Thr Gly		
149	1 5 10 15		
151	Ala Leu Ala Phe Pro Ala Gly Asn Ala Thr Glu Leu Glu Lys Arg Gln		
152	20 25 30		
154	Thr Thr Pro Asn Ser Glu Gly Trp His Asp Gly Tyr Tyr Ser Trp		
155	35 40 45		
157	Trp Ser Asp Gly Gly Ala Gln Ala Thr Tyr Thr Asn Leu Glu Gly Gly		
158	50 55 60		
160	Thr Tyr Glu Ile Ser Trp Gly Asp Gly Gly Asn Leu Val Gly Gly Lys		
161	65 70 75 80		
163	Gly Trp Asn Pro Gly Leu Asn Ala Arg Ala Ile His Phe Glu Gly Val		
164	85 90 95		
166	Tyr Gln Pro Asn Gly Asn Ser Tyr Leu Ala Val Tyr Gly Trp Thr Arg		
167	100 105 110		
169	Asn Pro Leu Val Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr Asp		
170	115 120 125		
172	Pro Ser Ser Gly Ala Thr Asp Leu Gly Thr Val Glu Cys Asp Gly Ser		
173	130 135 140		
175	Ile Tyr Arg Leu Gly Lys Thr Thr Arg Val Asn Ala Pro Ser Ile Asp		
176	145 150 155 160		
178	Gly Thr Gln Thr Phe Asp Gln Tyr Trp Ser Val Arg Gln Asp Lys Arg		
179	165 170 175		
181	Thr Ser Gly Thr Val Gln Thr Gly Cys His Phe Asp Ala Trp Ala Arg		
182	180 185 190		
184	Ala Gly Leu Asn Val Asn Gly Asp His Tyr Tyr Gln Ile Val Ala Thr		
185	195 200 205		
187	Glu Gly Tyr Phe Ser Ser Gly Tyr Ala Arg Ile Thr Val Ala Asp Val		
188	210 215 220		
190	Gly		
191	225		

VERIFICATION SUMMARY

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:36 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1) (vi)